



STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: US/08/113,646A  
FILING DATE: 31-AUG-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICANT: US 07/084,406  
FILING DATE: 10-AUG-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-20  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
US-08-113-646A-44

Query Match 1.5%; Score 32; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
DB 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 3  
US-09-720-201A-19/c  
Sequence 19, Application US/09720201A  
Patent No. 6524853  
GENERAL INFORMATION:  
APPLICANT: KOHARA, MICHINORI  
APPLICANT: KOHARA, KYOKO  
APPLICANT: TAIRA, KAZUNARI  
APPLICANT: MATSUZAKI, JUNICHI  
APPLICANT: OHMORI, HIROSHI  
TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND  
FILE REFERENCE: 04853.0051-00000  
CURRENT APPLICATION NUMBER: US/09/720,201A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: JP 98/177,820  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: PCT/JP99/03381  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 38  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-720-201A-19

Query Match 1.5%; Score 32; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 4  
US-08-771-624B-1/c  
Sequence 1, Application US/08771624B  
Patent No. 5914230  
GENERAL INFORMATION:  
APPLICANT: Liu, Yen Ping  
APPLICANT: Patel, Rajesh D.  
APPLICANT: Kurn, Nurith  
APPLICANT: Lin, Claire  
APPLICANT: Rose, Samuel J.  
APPLICANT: Ullman, Edwin F.  
TITLE OF INVENTION: Homogeneous Amplification and Detection  
TITLE OF INVENTION: of Nucleic Acids  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Behring Diagnostics GmbH, c/o Dade Behring Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: US  
ZIP: 60015-0778  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/771,624B  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,090  
FILING DATE: 22-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ruzsala, Lois K.  
REGISTRATION NUMBER: 39,074  
REFERENCE/DOCKET NUMBER: 1030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 267-5364  
TELEFAX: (847) 267-6024  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: C-terminal  
US-08-771-624B-1

Query Match 1.5%; Score 32; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
DB 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 5  
US-08-440-209-4/c  
Sequence 4, Application US/08440209

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; Patent No. 5922857
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,209
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,895
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-440-209-4

Query Match 1.5%; Score 32; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 6
US-08-439-996-4/c
; Sequence 4, Application US/08439996
; Patent No. 6057093
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,996
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,895A
; FILING DATE:
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-439-996-4

Query Match 1.5%; Score 32; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
| | | | | | | | | | | | | | | | | | | | | |
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 7
US-09-732-067-7
; Sequence 7, Application US/09732067
; Patent No. 6457426
; GENERAL INFORMATION:
; APPLICANT: Ullman, Edwin
; APPLICANT: Singh, Rajendra
; APPLICANT: DeKeczer, Steve
; APPLICANT: Davalian, Dariush
; TITLE OF INVENTION: Amplified Luminescent Homogeneous
; FILE REFERENCE: BEH-7385
; CURRENT APPLICATION NUMBER: US/09/732,067
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hybridization oligo
; US-09-732-067-7

Query Match 1.5%; Score 32; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32
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## RESULT 8

US-08-420-443-1  
; Sequence 1, Application US/08420443  
; Patent No. 5607834  
; GENERAL INFORMATION:  
; GENERAL INFORMATION:  
; APPLICANT: C. Bruce Bagwell  
; TITLE OF INVENTION: NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/420,443  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/990,298  
; FILING DATE: 19921210  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Y. Rocky Tsao  
; REGISTRATION NUMBER: 34,053  
; REFERENCE/DOCKET NUMBER: 05663/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-420-443-1

Query Match 1.5%; Score 32; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 32: Conservative 0; Mismatches 0; Indels

[illegible]

## RESULT 9

US-09-621-976-14612  
; Sequence 14612, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 14612  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-14612

Query Match 1.5%; Score 32; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 32; Conservative 0; Mismatches 0; Indels

QY	2067	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2098
pb	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	32

## RESULT 10

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US-09-621-976-14715
; Sequence 14715, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14715
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14715

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Query Match 1.5%; Score 32; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 32; Conservative 0; Mismatches 0; Indels

Qy	2067	2098
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pb	1	32
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## RESULT 11

US-09-197-814-9/c  
; Sequence 9, Application US/09197814A  
; Patent No. 6316220  
; GENERAL INFORMATION:  
; APPLICANT: Christensen, Tove  
; TITLE OF INVENTION: A transcription factor  
; FILE REFERENCE: 4484.204-US  
; CURRENT APPLICATION NUMBER: US/09/197,814A  
; CURRENT FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: 0740/96  
; EARLIER FILING DATE: 1996-07-05  
; EARLIER APPLICATION NUMBER: PCT/DK97/003035  
; EARLIER FILING DATE: 1997-07-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-197-814-9

Query Match 1.5%; Score 31; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0.00055;  
Matches 31; Conservative 0; Mismatches 0; Indels

Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2097  
 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11  
 pb

RESULT 12

REPORT 12  
US-09-920-581-9/c



Qy	2067	2097
Qy	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA
Db	43	13
	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA

Search completed: July 2, 2004, 07:38:41  
Job time : 158 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:36:20 ; Search time 1830 Seconds  
(without alignments)  
5530.704 Million cell updates/sec

Title: US-09-445-223-2  
Perfect score: 2098  
Sequence: 1 ggccattatggatgggg.....aaaaaaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3163042 seqs, 2412103800 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1726952

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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16:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-Result No.	Score	Query Match	Length	DB ID	Description
1	50	2.4	50	16	US-10-131-827-4651
C 2	34	1.6	45	9	US-09-827-289-14
C 3	34	1.6	45	9	US-09-827-289-18
C 4	34	1.6	46	9	US-09-827-289-21
C 5	34	1.6	46	9	US-09-827-289-25
6	33	1.6	36	9	US-09-828-034-2
7	33	1.6	36	9	US-09-828-034-3
C 8	33	1.6	46	9	US-09-827-289-22
C 9	33	1.6	46	9	US-09-827-289-26
C 10	32	1.5	32	15	US-10-371-600-2
C 11	32	1.5	32	15	US-10-371-600-9
C 12	32	1.5	32	15	US-10-371-600-10
C 13	32	1.5	38	10	US-09-764-891-10175
C 14	32	1.5	39	15	US-10-289-921-6

C 15	32	1.5	40	13	US-10-463-549-26	Sequence 26, Appl
C 16	32	1.5	43	15	US-10-218-567-7	Sequence 7, Appl
C 17	32	1.5	43	15	US-10-352-253A-37	Sequence 37, Appl
18	32	1.5	47	10	US-09-764-891-10177	Sequence 10177, A
C 19	32	1.5	47	15	US-10-289-921-5	Sequence 5, Appl
C 20	32	1.5	48	17	US-10-062-188-107	Sequence 107, Appl
C 21	32	1.5	48	17	US-10-668-749A-4	Sequence 4, Appl
C 22	32	1.5	50	9	US-09-815-343-1012	Sequence 1012, Ap
C 23	32	1.5	50	13	US-10-097-105-1012	Sequence 1012, Ap
C 24	31	1.5	41	9	US-09-920-581-9	Sequence 9, Appl
C 25	31	1.5	41	15	US-10-371-421-9	Sequence 9, Appl
C 26	31	1.5	43	10	US-09-932-165-1485	Sequence 1485, Ap
C 27	31	1.5	43	10	US-09-942-052-714	Sequence 714, App
C 28	31	1.5	43	13	US-10-013-312-2995	Sequence 2995, Ap
C 29	31	1.5	43	13	US-10-087-190-30	Sequence 30, Appl
C 30	31	1.5	43	15	US-10-121-019-13	Sequence 13, Appl
C 31	31	1.5	43	16	US-10-120-885A-28	Sequence 28, Appl
C 32	31	1.5	43	16	US-10-121-016-55	Sequence 55, Appl
C 33	31	1.5	43	16	US-10-114-669-6	Sequence 42, Appl
C 34	31	1.5	43	16	US-10-114-432-42	Sequence 42, Appl
C 35	31	1.5	45	10	US-09-894-916-3	Sequence 3, Appl
36	30	1.4	30	13	US-09-880-727-10	Sequence 10, Appl
C 37	30	1.4	30	13	US-10-314-578-1094	Sequence 1094, Ap
38	30	1.4	30	13	US-10-314-578-1095	Sequence 1095, Ap
C 39	30	1.4	30	14	US-10-042-193A-1	Sequence 1, Appl
40	30	1.4	30	14	US-10-042-193A-2	Sequence 2, Appl
C 41	30	1.4	30	16	US-10-380-584-115	Sequence 115, App
C 42	30	1.4	32	15	US-10-371-600-3	Sequence 3, Appl
C 43	30	1.4	32	15	US-10-371-600-4	Sequence 4, Appl
C 44	30	1.4	39	15	US-10-219-195-28	Sequence 28, Appl
C 45	30	1.4	39	15	US-10-219-195-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-10-131-827-4651  
; Sequence 4651, Application US/10131827  
; Publication No. US2004009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4651  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-4651

Query Match 2.4%; Score 50; DB 16; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e-14;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1803 TGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCT 1852  
Db 1 TGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCT 50

RESULT 2  
US-09-827-289-14/c





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; SEQ ID NO 2
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-2

Query Match      1.6%; Score 33; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 7
US-09-828-034-3
; Sequence 3, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-3

Query Match      1.6%; Score 33; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 8
US-09-827-289-22/c
; Sequence 22, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-22
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Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 9
US-09-827-289-26/c
; Sequence 26, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-26

Query Match      1.6%; Score 33; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 10
US-10-371-600-2/c
; Sequence 2, Application US/10371600
; Publication No. US20030180776A1
; GENERAL INFORMATION:
; APPLICANT: WU, MING
; APPLICANT: ULLMAN, EDWIN F.
; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION
; FILE REFERENCE: 3817.10-2
; CURRENT APPLICATION NUMBER: US/10/371,600
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/359,223
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/379,360
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-371-600-2

Query Match      1.5%; Score 32; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11  
US-10-371-600-9  
; Sequence 9, Application US/10371600  
; Publication No. US20030180776A1  
; GENERAL INFORMATION:  
; APPLICANT: WU, MING  
; APPLICANT: ULLMAN, EDWIN F.  
; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION  
; FILE REFERENCE: 3817.10-2  
; CURRENT APPLICATION NUMBER: US/10/371,600  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: 60/359,223  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/379,360  
; PRIOR FILING DATE: 2002-05-08  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide  
US-10-371-600-9

Query Match 1.5%; Score 32; DB 15; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 12  
US-10-371-600-10/c  
; Sequence 10, Application US/10371600  
; Publication No. US20030180776A1  
; GENERAL INFORMATION:  
; APPLICANT: WU, MING  
; APPLICANT: ULLMAN, EDWIN F.  
; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION  
; FILE REFERENCE: 3817.10-2  
; CURRENT APPLICATION NUMBER: US/10/371,600  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: 60/359,223  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/379,360  
; PRIOR FILING DATE: 2002-05-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide  
US-10-371-600-10

Query Match 1.5%; Score 32; DB 15; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13  
US-09-764-891-10175  
; Sequence 10175, Application US/09764891  
; Publication No. US20030077808A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC006  
; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10175  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-891-10175

Query Match 1.5%; Score 32; DB 10; Length 38;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 14  
US-10-289-921-6/c  
; Sequence 6, Application US/10289921  
; Publication No. US20030113337A1  
; GENERAL INFORMATION:  
; APPLICANT: MERUELO, Daniel  
; APPLICANT: OHNO, Kouichi  
; APPLICANT: LEVIN, Brandi A.  
; TITLE OF INVENTION: HIGH EFFICIENCY TISSUE SPECIFIC COMPOUND  
; FILE REFERENCE: 5986/11123-US1  
; CURRENT APPLICATION NUMBER: US/10/289,921  
; CURRENT FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: US 08/566,421  
; PRIOR FILING DATE: 1995-11-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: biotinylated poly(dT) oligonucleotide  
US-10-289-921-6

Query Match 1.5%; Score 32; DB 15; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 15  
US-10-463-549-26/c  
; Sequence 26, Application US/10463549  
; Publication No. US20040053308A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Kumi  
; TITLE OF INVENTION: Probe Immobilized Substrate and Method for Manufacturing the Same  
; FILE REFERENCE: 03560.003309



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 2098  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
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25: em\_gss\_rod:\*  
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27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	35	1.7	50	AA564185	AA564185 nj04dl1.s

C	5	34	1.6	40	14	CF332441	CF332441 NACL--08-
C	6	33	1.6	33	13	BU431798	BU431798 601655890
C	7	33	1.6	34	13	BU431799	BU431799 601655967
C	8	33	1.6	39	14	CF327755	CF327755 NACL--02-
C	9	33	1.6	40	2	HSM001841	AL037510 Homo sapi
C	10	33	1.6	44	14	CF302212	CF302212 7LEAF--07
C	11	33	1.6	44	14	CF305473	CF305473 CLD1--01-
C	12	33	1.6	44	14	CF334384	CF334384 JMT--03-K
C	13	33	1.6	45	10	BF582680	BF582680 602094085
C	14	33	1.6	46	13	BF582680	BF582680 602094085
C	15	33	1.6	46	14	CF332152	CF332152 NACL--08-
C	16	33	1.6	47	14	CF3337040	CF3337040 JMT--07-F
C	17	33	1.6	48	14	CF333983	CF333983 JMT--03-B
C	18	33	1.6	49	9	AA852759	AA852759 NHTBCael5
C	19	33	1.6	49	9	AI316598	AI316598 uk62a04.y
C	20	33	1.6	49	28	AZ587341	AZ587341 IM0394020
C	21	33	1.6	50	9	AA853120	AA853120 NHTBCae03
C	22	33	1.6	50	9	AA617223	AA617223 vj79e05.x
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C	25	33	1.6	50	13	BI496942	BI496942 df129g10.
C	26	33	1.6	50	13	BI496942	BI496942 df129g10.
C	27	33	1.6	50	13	BI496942	BI496942 df129g10.
C	28	32	1.5	32	10	AW327277	CA335626 NISC lu01
C	29	32	1.5	32	14	CF291773	AW327277 dq01d07.x
C	30	32	1.5	32	14	CF299386	CF291773 14ROOT--0
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C	32	32	1.5	32	14	CF309233	CF309233 ABF--03-F
C	33	32	1.5	32	14	CF309345	CF309345 ABF--03-I
C	34	32	1.5	32	14	CF313717	CF313717 HD--01-P0
C	35	32	1.5	32	14	CF321046	CF321046 HD--12-C1
C	36	32	1.5	32	14	CF328471	CF328471 NACL--03-
C	37	32	1.5	32	14	CF331270	CF331270 NACL--07-
C	38	32	1.5	32	28	AZ459536	AZ459536 1M0264M16
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C	41	32	1.5	32	28	AZ778018	AZ778018 2M0012O20
C	42	32	1.5	32	29	DR85L21T	AL986044 Danio rer
C	43	32	1.5	33	9	AL587609	AL587609 AL587609
C	44	32	1.5	33	14	CF291613	CF291613 14ROOT--0
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ALIGNMENTS

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AU106827  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

50 bp mRNA linear EST 30-AUG-2001  
AU106827 Sugano Homo sapiens cdna library Homo sapiens cdna clone  
HEP20988, mRNA sequence.  
AU106827  
AU106827.1 GI:13556348  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and



Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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1. .50  
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/clone="HEP20988"  
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QY 20 GCGGCGCTACGGCGTTGGCACCAGTCTCTAGAAAAGAGTCAG 62  
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Db 8 GCGGCGCTACGGCGTTGGCACCAGTCTCTAGAAAAGAGTCAG 50

RESULT 2  
AUI06825  
LOCUS  
DEFINITION  
AUI06825 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
CAS01421, mRNA sequence.  
ACCESSION  
VERSION  
AUI06825.1 GI:13556346  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,  
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,  
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
PUBMED  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and  
Sugano,S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GTCAGCTCTGGTTCGGAGAGCAGCGGTGGCGTGGGCCAT 98  
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RESULT 3  
AUI06826  
LOCUS  
DEFINITION  
AUI06826 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
CAS03470, mRNA sequence.  
AUI06826  
VERSION  
AUI06826.1 GI:13556347  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,  
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,  
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
PUBMED  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and  
Sugano,S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

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ORIGIN

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Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 GTCTCTAGAAAAGATCAGCTCTGGTTCCGAGAACGACG 50

RESULT 4  
AA564185/c  
LOCUS  
DEFINITION  
AA564185 50 bp mRNA linear EST 04-SEP-1997  
nJ04d11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone IMAGE:985365 3',  
mRNA sequence.  
ACCESSION  
VERSION  
AA564185.1 GI:2335824  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 50)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 203 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham.

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with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is not normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 50;  
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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2064 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 44 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 10

RESULT 5  
CF332441/c  
LOCUS  
DEFINITION  
NACL--08-P05.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-P05, mRNA sequence.  
CF332441  
EST.  
CF332441.1 GI:33813099  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 40)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/clone\_lib="Rice callus plasmid cDNA library (NACL) "  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

ORIGIN

Query Match 1.6%; Score 34; DB 14; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2063 TTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2096  
Db 34 TTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 6  
BU431798/c  
LOCUS  
DEFINITION  
BU431798  
601655890R1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3855694 3',  
mRNA sequence.  
BU431798  
EST.  
BU431798.1 GI:22770280  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 33)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM570 row: c column: 23  
High quality sequence stop: 31.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3855694"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_66"  
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.8 kb. Library constructed by Life  
Technologies. "

ORIGIN

Query Match 1.6%; Score 33; DB 13; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 33 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 7  
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DEFINITION  
BU431799  
601655967R1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3855737 3',  
mRNA sequence.  
BU431799  
EST.  
BU431799.1 GI:22770281  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 34)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCM570 row: e column: 18 High quality sequence stop: 31. Location/Qualifiers															
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ACCESSION      CF302212
VERSION        CF302212.1  GI:33673973
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 44)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES       Location/Qualifiers
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               /organism="Oryza sativa"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:4530"
               /clone="7LEAF-07-I14"
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               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

ORIGIN
Query Match      1.6%; Score 33; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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Db      37 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 11
CF305473/c
LOCUS
DEFINITION      CF305473 44 bp mRNA linear EST 15-AUG-2003
                 CLD1--01-M22.b1 Rice cold treated leaf plasmid cDNA library (CLD1)
                 Oryza sativa cDNA clone CLD1--01-M22, mRNA sequence.
ACCESSION      CF305473
VERSION        CF305473.1  GI:33677234
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 44)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES       Location/Qualifiers
               1..44
               /organism="Oryza sativa"
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mol_type="mRNA"
cultivar="Nackdong"
db_xref="taxon:4530"
clone="CLD1--01-M22"
tissue_type="leaf"
dev_stage="14 days after germination"
lab_host="E.coli DH10B"
clone_lib="Rice cold treated leaf plasmid cDNA library
(CL D1)"
note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was
incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
mRNA was reverse transcribed and then used for PCR."

ORIGIN
Query Match      1.6%; Score 33; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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         |||||
Db      39 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 12
CF334384/c
LOCUS
DEFINITION      CF334384 44 bp mRNA linear EST 18-AUG-2003
                 JMT--03-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
                 library (JMT) Oryza sativa cDNA clone JMT--03-K14, mRNA sequence.
ACCESSION      CF334384
VERSION        CF334384.1  GI:33817097
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 44)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES       Location/Qualifiers
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               /tissue_type="leaf"
               /dev_stage="14 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="AtJMT-overexpressing transgenic rice plasmid
               cDNA library (JMT)"
               /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
               was reverse transcribed and then used for PCR. mRNA was
               prepared from Arabidopsis Jasmoinate Carboxyl
               methyltransferase overexpression line."
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ORIGIN
Query Match      1.6%; Score 33; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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Db      42 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 10
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RESULT 13
BF582680
LOCUS
DEFINITION
BF582680
BF582680
BF582680.1 GI:11656398
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9772 row: j column: 22
High quality sequence stop: 45.
FEATURES
Location/Qualifiers
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/strain="FVB/N"
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/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 1.6%; Score 33; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
|||||
DB 6 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 38
RESULT 14
BX561724
LOCUS
DEFINITION
BX561724 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse57d10_glc, mRNA sequence.
BX561724
BX561724.1 GI:33371526
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 46)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL
Genome Biol 4 (10), R63 (2003)

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

ORIGIN

Query Match 1.6%; Score 33; DB 14; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
|||  
Db 11 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 43

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Job time : 5412 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:25:14 ; Search time 8116 Seconds  
(without alignments)  
11204.249 Million cell updates/sec

Title: US-09-445-223-2  
Perfect score: 2098  
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Gapop 60.0 , Gapext 60.0  
Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl:

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- 2: gb\_htg:\*
- 3: gb\_in:\*
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- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
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- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	34	1.6	45	6	AX287571	AX287571 Sequence
C 2	34	1.6	45	6	AX287575	AX287575 Sequence
C 3	34	1.6	46	6	AX287578	AX287578 Sequence
C 4	34	1.6	46	6	AX287582	AX287582 Sequence
C 5	33	1.6	46	6	AX287579	AX287579 Sequence
C 6	33	1.6	46	6	AX287583	AX287583 Sequence
C 7	33	1.6	49	6	E62856	E62856 Secretary p
C 8	32	1.5	33	6	BD011883	BD011883 Detection
C 9	32	1.5	37	6	I29931	I29931 Sequence 44
C 10	32	1.5	37	6	AX106972	AX106972 Sequence
C 11	32	1.5	38	6	E50766	E50766 Vector expr
C 12	32	1.5	40	6	A48799	A48799 Sequence 6
C 13	32	1.5	40	6	AR232955	AR232955 Sequence
C 14	32	1.5	43	6	AX225198	AX225198 Sequence
C 15	32	1.5	44	6	AX206861	AX206861 Sequence
C 16	32	1.5	45	6	E50989	E50989 Method for
C 17	32	1.5	50	6	I36502	I36502 Sequence 1
C 18	32	1.5	50	6	AR423115	AR423115 Sequence
C 19	32	1.5	50	6	AR423218	AR423218 Sequence
C 20	32	1.5	50	6	AX261361	AX261361 Sequence
C 21	32	1.5	50	6	BD118668	BD118668 EST and e
C 22	32	1.5	50	6	BD118771	BD118771 EST and e
C 23	32	1.5	50	6	BD170451	BD170451 Method of
C 24	31	1.5	41	6	AR309630	AR309630 Sequence
C 25	31	1.5	43	6	AX395321	AX395321 Sequence
C 26	31	1.5	43	6	AX443022	AX443022 Sequence
C 27	31	1.5	43	6	AX459616	AX459616 Sequence
C 28	31	1.5	44	6	AR038858	AR038858 Sequence
C 29	31	1.5	45	6	AR429142	AR429142 Sequence
C 30	31	1.5	45	6	AX838339	AX838339 Sequence
C 31	31	1.5	45	6	AX840840	AX840840 Sequence
C 32	31	1.5	45	6	BD016445	BD016445 Gene deri
C 33	31	1.5	50	6	BD132852	BD132852 Methods O
C 34	30	1.4	30	6	A43784	A43784 Sequence 9
C 35	30	1.4	30	6	A62991	A62991 Sequence 3
C 36	30	1.4	30	6	A62995	A62995 Sequence 7
C 37	30	1.4	30	6	AR179066	AR179066 Sequence
C 38	30	1.4	30	6	AR179070	AR179070 Sequence
C 39	30	1.4	30	6	E04638	E04638 Synthesized
C 40	30	1.4	30	6	I84450	I84450 Sequence 9
C 41	30	1.4	30	6	AX104902	AX104902 Sequence
C 42	30	1.4	30	6	AX104903	AX104903 Sequence
C 43	30	1.4	30	6	AX474673	AX474673 Sequence
C 44	30	1.4	30	6	AX474674	AX474674 Sequence
C 45	30	1.4	30	6	AX521609	AX521609 Sequence

ALIGNMENTS

RESULT 1  
AX287571/c  
LOCUS AX287571 45 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 14 from Patent WO0177390.  
ACCESSION AX287571  
VERSION AX287571.1 GI:17049337  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS abarz A.P.  
TITLE Process for allele discrimination utilizing primer extension  
JOURNAL Patent: WO 0177390-A 14 18-OCT-2001;  
Molecular Staging, Inc. (US)

Qy	Db	Sequence	Score	DB 6;	Length	Indels	Mismatches	Gaps
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34	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1						
<p>RESULT 4</p> <p>AX287582/c</p> <p>LOCUS AX287582 46 bp DNA linear PAT 21-NOV-2001</p> <p>DEFINITION Sequence 25 from Patent WO0177390.</p> <p>ACCESSION AX287582</p> <p>VERSION AX287582.1 GI:17049348</p> <p>KEYWORDS .</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS abarz A,P.</p> <p>TITLE Process for allele discrimination utilizing primer extension</p> <p>JOURNAL Patent: WO 0177390-A 25 18-OCT-2001;</p> <p>MOLECULAR STAGING, INC. (US)</p> <p>FEATURES</p> <p>source</p> <p>1. .46</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="P1 primer for use in allele discrimination"</p> <p>ORIGIN</p> <p>Query Match 1.6%; Score 34; DB 6; Length 46;</p> <p>Best Local Similarity 100.0%; Pred. No. 9e-07;</p> <p>Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>								
2065	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2098						
34	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1						
<p>RESULT 5</p> <p>AX287579/c</p> <p>LOCUS AX287579 46 bp DNA linear PAT 21-NOV-2001</p> <p>DEFINITION Sequence 22 from Patent WO0177390.</p> <p>ACCESSION AX287579</p> <p>VERSION AX287579.1 GI:17049345</p> <p>KEYWORDS .</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS abarz A,P.</p> <p>TITLE Process for allele discrimination utilizing primer extension</p> <p>JOURNAL Patent: WO 0177390-A 22 18-OCT-2001;</p> <p>MOLECULAR STAGING, INC. (US)</p> <p>FEATURES</p> <p>source</p> <p>1. .46</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="P1 primer for use in allele discrimination"</p> <p>ORIGIN</p> <p>Query Match 1.6%; Score 33; DB 6; Length 46;</p> <p>Best Local Similarity 100.0%; Pred. No. 3.2e-06;</p> <p>Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>								
2065	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2098						
34	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1						
<p>RESULT 6</p> <p>AX287582/c</p> <p>LOCUS AX287582 46 bp DNA linear PAT 21-NOV-2001</p> <p>DEFINITION Sequence 25 from Patent WO0177390.</p> <p>ACCESSION AX287582</p> <p>VERSION AX287582.1 GI:17049348</p> <p>KEYWORDS .</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS abarz A,P.</p> <p>TITLE Process for allele discrimination utilizing primer extension</p> <p>JOURNAL Patent: WO 0177390-A 25 18-OCT-2001;</p> <p>MOLECULAR STAGING, INC. (US)</p> <p>FEATURES</p> <p>source</p> <p>1. .46</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="P1 primer for use in allele discrimination"</p> <p>ORIGIN</p> <p>Query Match 1.6%; Score 33; DB 6; Length 46;</p> <p>Best Local Similarity 100.0%; Pred. No. 3.2e-06;</p> <p>Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>								
2065	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2098						
34	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1						

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'AX287583/c
LOCUS      AX287583
DEFINITION Sequence 26 from Patent WO0177390.
ACCESSION  AX287583
VERSION     AX287583.1 GI:17049349
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     abaraz A,P.
TITLE       Process for allele discrimination utilizing primer extension
JOURNAL     Patent: WO 0177390-A 26 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES    Location/Qualifiers
             source
             1..46
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="P1 primer for use in allele discrimination"
ORIGIN
Query Match      1.6%; Score 33; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
      |||||||||||||||||||||||||||||||||||||||
Db 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 7
E62856
LOCUS      E62856
DEFINITION Secretory protein.
ACCESSION  E62856
VERSION     E62856.1 GI:22562584
KEYWORDS    JP 2001509004-A/14.
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE   1 (bases 1 to 49)
AUTHORS     Jacobs,K., McCoy,J.M., Racie,L.A., Lavallie,E.R., Merberg,D. and
            Spaulding,V.
TITLE       Secretory protein
JOURNAL     Patent: JP 2001509004-A 14 10-JUL-2001;
            GENETICS INSTITUTE INC
COMMENT     PN JP 2001509004-A/14
            PD 10-JUL-2001
            PF 14-APR-1997 JP 1997537270
            PR 18-APR-1996 US 08/634325
            PI KENNETH JACOBS,JOHN M MCCOY,LISA A RACIE,EDWARD R LAVALLIE, PI
            DAVID MERBERG,
            PI VIKKI SPAULDING
            PC C12N15/12,C07K14/47,A61K38/17
            CC Strandedness: Double;
            CC Topology: Linear;
FEATURES    Location/Qualifiers
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             1..49
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             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
ORIGIN
Query Match      1.6%; Score 33; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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Db 4 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36
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```
RESULT 8
BD011883/c
LOCUS      BD011883
DEFINITION Detection kit for SRSV.
ACCESSION  BD011883
VERSION     BD011883.1 GI:22092072
KEYWORDS    WO 0079280-A/13.
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 33)
REFERENCE   1
AUTHORS     Takeda,N., Natori,K., Miyamura,T., Kunio, Kamata, Sato,T. and
            Sato,S.
TITLE       Detection kit for SRSV
JOURNAL     Patent: WO 0079280-A 13 28-DEC-2000;
            JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE,MITSUAKI
            MORIGUCHI,KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD,NAOKAZU
            TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO KAMATA,TOSHINORI
            SATO,SEIYA SATO
COMMENT     OS Artificial Sequence
            PN WO 0079280-A/13
            PD 28-DEC-2000
            PF 22-JUN-2000 WO 2000JP004095
            PR 22-JUN-1999 JP 99P 175928
            PI NAOKAZU TAKEDA,KATSURO NATORI,TATSUO MIYAMURA,KUNIO PI
            KAMATA,TOSHINORI SATO,
            PI SEIYA SATO
            PC GOIN33/569,C12N15/40
            CC
FEATURES    Location/Qualifiers
             source
             1..33
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
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Query Match      1.5%; Score 32; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
      |||||||||||||||||||||||||||||||||||||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 9
I29931
LOCUS      I29931
DEFINITION Sequence 44 from patent US 5578468.
ACCESSION  I29931
VERSION     I29931.1 GI:1820722
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 37)
AUTHORS     Pickup,D.J., Patel,D. and Antczak,J.B.
TITLE       Site-specific RNA cleavage
JOURNAL     Patent: US 5578468-A 44 26-NOV-1996;
            Location/Qualifiers
FEATURES    source
             1..37
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN
Query Match      1.5%; Score 32; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
      |||||||||||||||||||||||||||||||||||||||
```



```

1.5%; Score 32; DB 6; Length 38;
Best Local Similarity
100.0%; Pred. No. 1.1e-05;

```

VERSION AX225198.1 GI:15555219  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Schouten, J.P.  
 TITLE Multiplex ligatable probe amplification  
 JOURNAL Patent: WO 0161033-A 7 23-AUG-2001;  
 Schouten, Johannes Petrus (NL)  
 FEATURES Location/Qualifiers  
 source 1..43  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="synthetic DNA"  
 ORIGIN

Query Match 1.5%; Score 32; DB 6; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12

RESULT 15  
 AX206861/c  
 LOCUS AX206861 44 bp DNA linear PAT 30-AUG-2001  
 DEFINITION Sequence 7 from Patent WO0155391.  
 ACCESSION AX206861  
 VERSION AX206861.1 GI:15394685  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Jakobovits, A., Afar, D.E., Challita-Eid, P.M., Levin, E.,  
 Mitchell, S.C. and Hubert, R.S.  
 TITLE 84p2a9: a prostate and testis specific protein highly expressed in  
 JOURNAL prostate cancer  
 Patent: WO 0155391-A 7 02-AUG-2001;  
 Urogenesys, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..44  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"  
 ORIGIN

Query Match 1.5%; Score 32; DB 6; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 44 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13

Search completed: July 2, 2004, 06:05:40  
 Job time : 8130 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

\*OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:23:53 ; Search time 822 Seconds  
(without alignments)  
10842.725 Million cell updates/sec

Title: US-09-445-223-2  
Perfect score: 2098  
Sequence: 1 ggccattatggtgatggg.....aaaaaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3185356

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	50	2.4	50	6	ABZ04660	Abz04660 Human leu
C 2	34	1.6	45	6	AAS95728	Aas95728 Allele di
C 3	34	1.6	45	6	AAS95724	Aas95724 Allele di
C 4	34	1.6	46	6	AAS95735	Aas95735 Allele di
C 5	34	1.6	46	6	AAS95731	Aas95731 Allele di
6	33	1.6	36	6	ABK99273	Abk99273 Hepatitis
7	33	1.6	36	6	ABK99272	Abk99272 Hepatitis
8	33	1.6	36	6	AAD27116	Aad27116 RNA templ
9	33	1.6	36	6	AAD27117	Aad27117 RNA templ
10	33	1.6	37	6	AAD27125	Aad27125 RNA templ
C 11	33	1.6	46	6	AAS95732	Aas95732 Allele di
C 12	33	1.6	46	6	AAS95736	Aas95736 Allele di
13	33	1.6	49	2	AAV02146	Aav02146 Human sec
14	33	1.6	49	2	AAT88080	Aat88080 3' portio
C 15	32	1.5	32	1	AAN70278	Aan70278 Sequence
C 16	32	1.5	32	1	AAN92244	Aan92244 SS probe
C 17	32	1.5	32	9	ADC33445	Adc33445 Template
C 18	32	1.5	33	5	AAF29153	Aaf29153 PCR prime
C 19	32	1.5	38	3	AAZ57404	Aaz57404 Hepatitis
20	32	1.5	38	4	AAI07487	Aai07487 Human rep
C 21	32	1.5	40	2	AAQ25031	Aaq25031 Oligonuc
C 22	32	1.5	40	3	AAZ98722	Aaz98722 PCR prime
C 23	32	1.5	40	3	AAA39649	Aaa39649 Primer us

C	24	32	1.5	43	4	AAD17216	Aad17216 Human mRN
25	32	32	1.5	44	2	AAV09273	Aav09273 Nucleotid
C 26	32	32	1.5	44	5	AAS11665	Aas11665 Prostate
C 27	32	32	1.5	44	9	ADD33791	Add33791 Mouse mit
28	32	32	1.5	45	4	AAF26960	Aaf26960 Primer fo
29	32	32	1.5	47	4	AAI07489	Aai07489 Human rep
C 30	32	32	1.5	48	2	AAT04081	Aat04081 Trypsin i
31	32	32	1.5	48	6	ABK30210	Abk30210 CYP2D6 ge
C 32	32	32	1.5	48	9	ADD31868	Add31868 Butterfly
33	32	32	1.5	50	2	AAQ66922	Aaq66922 Poly-da 5
C 34	32	32	1.5	50	2	AAV37933	Aav37933 Primer of
35	32	32	1.5	50	4	AAF60897	Aaf60897 Conjugate
C 36	32	32	1.5	50	4	AAS58336	Aas58336 CDNA #101
37	32	32	1.5	50	6	ABK30194	Abk30194 CYP2D6 ge
C 38	32	32	1.5	50	6	ABN89414	Abn89414 Polymorph
C 39	32	32	1.5	50	7	ABQ77278	Abq77278 Oligo dt
C 40	32	32	1.5	50	7	ADA18497	Ada18497 Anchor po
C 41	32	32	1.5	50	9	ADC56860	Adc56860 Micro gol
C 42	32	32	1.5	50	9	ADC56857	Adc56857 Micro gol
43	32	32	1.5	50	9	ADC56856	Adc56856 Micro gol
44	31	31	1.5	37	6	AAD27124	Aad27124 RNA templ
C 45	31	31	1.5	41	2	AAV03013	Aav03013 Aspergill

ALIGNMENTS

RESULT 1  
ABZ04660  
ID ABZ04660 standard; DNA; 50 BP.  
XX  
AC ABZ04660;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE Human leukocyte gene expression profiling probe SEQ ID NO 4651.  
XX  
KW T7; leukocyte; gene expression profiling; allograft rejection;  
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200257414-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 22-OCT-2001; 2001WO-US047856.  
XX  
PR 20-OCT-2000; 2000US-0241994P.  
PR 08-JUN-2001; 2001US-0296764P.  
XX  
PA (BIOC-) BIOCARDIA INC.  
XX  
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
PI Ly N, Woodward R, Quettermous T, Johnson F;  
XX  
DR WPI; 2002-636525/68.  
XX  
PT New system for leukocyte expression profiling, diagnosing a disease, or  
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
PT or congestive heart failure, comprises diagnostic oligonucleotides.  
XX  
PS Claim 1; Page 476; Opp; English.  
XX  
CC The invention relates to a system for detecting gene expression, which  
CC comprises one or two isolated DNA molecules that detect expression of a  
CC gene, where the gene corresponds to any of 8143 oligonucleotides  
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
CC for leukocyte expression profiling. It is particularly useful for  
CC diagnosing a disease, monitoring (rate of) progression of a disease,  
CC predicting therapeutic outcome, determining prognosis for a patient,

CC predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX

SQ Sequence 50 BP; 10 A; 13 C; 10 G; 17 T; 0 U; 0 Other;

Query Match 2.4%; Score 50; DB 6; Length 50;

Best Local Similarity 100.0%; Pred. No. 3.2e-09;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1803 TGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCT 1852

Db 1 TGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCT 50

RESULT 2

AAS95728/c

ID AAS95728 standard; DNA; 45 BP.

XX

AC AAS95728;

XX

DT 14-FEB-2002 (first entry)

XX

DE Allele discrimination P1 primer #12.

XX

KW Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

XX

OS Homo sapiens.

XX

PN WO200177390-A2.

XX

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001WO-US011151.

XX

PR 05-APR-2000; 2000US-0194843P.

XX

PA (MOLE-) MOLECULAR STAGING INC.

XX

PI Abarzua P;

XX

DR WPI; 2002-049157/06.

XX

PT Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

XX

PS Claim 15; Page 41; 67pp; English.

XX

CC The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease deficient DNA polymerase enzyme under conditions that promote extension of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and melanoma. Sequences AAS95711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products

XX

SQ Sequence 45 BP; 2 A; 5 C; 0 G; 38 T; 0 U; 0 Other;

Query Match 1.6%; Score 34; DB 6; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0044;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2065 TGAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2098

Db 37 TGAAAAAATAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 3

AAS95724/c

ID AAS95724 standard; DNA; 45 BP.

XX

AC AAS95724;

XX

DT 14-FEB-2002 (first entry)

XX

DE Allele discrimination P1 primer #8.

XX

KW Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

XX

OS Homo sapiens.

XX

PN WO200177390-A2.

XX

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001WO-US011151.

XX

PR 05-APR-2000; 2000US-0194843P.

XX

PA (MOLE-) MOLECULAR STAGING INC.

XX

PI Abarzua P;

XX

DR WPI; 2002-049157/06.

XX

PT Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

XX

PS Claim 15; Page 41; 67pp; English.

XX

CC The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease deficient DNA polymerase enzyme under conditions that promote extension of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington



The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease deficient DNA polymerase enzyme under conditions that promote extension of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

Claim 15; Page 42; 67pp; English.

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (p1) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to p1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of p1 may not be complementary. The complex is then contacted with an exonuclease deficient DNA polymerase enzyme under conditions that promote extension of p1 with the target DNA as the template, thereby forming an extended segment of p1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

CC	templates	
XX	Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;	
SQL	Query Match 1.6%; Score 33; DB 6; Length 36;	
	Best Local Similarity 100.0%; Pred. No. 0.011;	
	Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098	
DB	2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34	
RESULT 7		
ABK99272		
ID	ABK99272 standard; RNA; 36 BP.	
XX		
AC	ABK99272;	
XX		
DT	21-OCT-2002 (first entry)	
XX		
DE	Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #2.	
XX		
KW	Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.	
XX		
OS	Synthetic.	
XX		
PN	US2002064771-A1.	
XX		
PD	30-MAY-2002.	
XX		
PF	06-APR-2001; 2001US-00828034.	
XX		
PR	07-APR-2000; 2000US-0195852P.	
XX		
PA	(ZHON/) ZHONG W.	
PA	(HONG/) HONG Z.	
PA	(FERR/) FERRARI E.	
XX		
PI	Zhong W, Hong Z, Ferrari E;	
XX		
DR	WPI; 2002-582330/62.	
XX		
PT	Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3	
PT	nucleotide-long template to which a 2 nucleotide-long primer is annealed,	
PT	and template and primer which do not form a stable duplex in the absence	
PT	of HCV NS5B.	
XX		
PS	Example; Page 6; 17pp; English.	
XX		
CC	The invention relates to a replicase complex comprising a hepatitis C	
CC	virus (HCV) NS5B replicase protein, a linear nucleic acid template and a	
CC	complementary nucleic acid primer which is annealed to the 3' terminus of	
CC	the template, where the template is at least three nucleotides and the	
CC	primer is two or three nucleotides, and the template and primer do not	
CC	form a stable duplex in solution in the absence of the HCV NS5B protein.	
CC	The complex is useful for detecting HCV replicase activity and permits	
CC	establishment of sensitive RNA-dependent RNA polymerase assays to screen	
CC	and evaluate antiviral inhibitors and to improve the specificity and	
CC	efficacy of the inhibitors. The complex is also useful in the development	
CC	of a reliable system for determining kinetic and thermodynamic constants	
CC	of HCV NS5B-catalysed nucleotide incorporation and investigation of	
CC	mechanistic inhibitors for mis-incorporation or chain termination.	
CC	Specifically, the short RNA template and primer pairs are useful in	
CC	screening assays which are used for determining kinetic, thermodynamic	
CC	and mechanistic properties of NS5B replication and ultimately in the	
CC	development of inhibitors of NS5B. Newly identified inhibitors of	
CC	replicase activity may be used for developing anti-HCV pharmaceuticals.	
CC	Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis	
XX	templates	
SQL	Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;	









XX EP227976-A.  
PN  
XX  
XX 08-JUL-1987.  
PD  
XX  
XX 04-DEC-1986; 86EP-00116906.  
PF  
XX  
XX 05-DEC-1985; 85US-00805279.  
PR  
XX  
XX (MEIO-) MEIOGENICS INC.  
PA  
XX  
XX Duck P, Bender R, Crosby W, Robertson JG;  
PI  
XX  
XX WPI; 1987-186567/27.  
DR  
XX  
XX Synthetic nucleic acid probes - comprising two nucleic acid sequences  
PT linked by a scissile linkage.  
PT  
XX  
XX Example; p29; 46pp; English.  
PS  
XX  
XX The patent claims a new molecule of formula (NA1---S---NA2)n. NA1 and  
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile  
CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA  
CC or RNA sequences in a test soln. The scissile link probes may be PL  
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid  
CC support). The differential liability of DNA and RNA may be exploited in a  
CC heterogeneous system when the scissile linkage is an RNA molecule. In the  
CC examples, counter probe molecules 9 through 16 were used to determine  
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing  
CC OS field.)  
XX  
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;  
Query Match 1.5%; Score 32; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1  
Search completed: July 2, 2004, 03:50:02  
Job time : 824 secs

DT 14-MAY-1998 (first entry)  
XX  
XX 3' portion of cDNA clone encoding secreted protein AK533.  
DE  
XX  
XX Human; secreted protein; research; treatment; AM533; 3' portion; ds.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9739122-A2.  
PN  
XX  
XX 23-OCT-1997.  
PD  
XX  
XX 11-APR-1997; 97WO-US0006042.  
PF  
XX  
XX 12-APR-1996; 96US-00631184.  
PR  
XX  
XX (MURO-) MURO PHARM INC.  
PA  
XX  
XX Theoharides TC;  
PI  
XX  
XX WPI; 1997-526459/48.  
DR  
XX  
XX Human and murine secreted proteins - useful in research or treatment of  
PT diseases or disorders related to their function.  
PT  
XX  
XX Disclosure; Page 86; 140pp; English.  
PS  
XX  
XX The present sequence is the 3' portion of a cDNA clone encoding a human  
CC secreted protein, which may have nutritional uses, or cytokine and cell  
CC proliferation/differentiation, immune stimulating or suppressing,  
CC haematopoiesis regulating, tissue growth, activin/inhibin,  
CC chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand,  
CC anti-inflammatory or tumour inhibition activities. It can also be used to  
CC research or treat diseases/disorders related to its function. The partial  
CC cDNA clone API62 was 1st isolated from a human adult placenta cDNA  
CC library. The partial cDNA clones AM931, AM610, AM340, AM282, AK647,  
CC AK583, AK533 and AK296 were 1st isolated from a human foetal kidney cDNA  
CC library. The partial cDNA clones H617 and BB9 were 1st isolated from a  
CC human peripheral blood monocyte cell (Th1 or Th2) cDNA library. The  
CC partial cDNA clone AW191 was 1st isolated from a human ovary (PA-1  
CC teratocarcinoma) cDNA library. The partial cDNA clones AT211, AT205 and  
CC AT319 were 1st isolated from a human lymphocyte and dendritic cell cDNA  
CC library. The partial cDNA clones AS34 and AS32 were 1st isolated from a  
CC human foetal brain cDNA library. The partial cDNA clone AR260 was 1st  
CC isolated from a human adult retina cDNA library. The partial cDNA clones  
CC K640 and K39 were 1st isolated from a murine bone marrow (stromal cell  
CC line FCM-4) cDNA library  
XX  
SQ Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 1.6%; Score 33; DB 2; Length 49;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
Db 4 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36  
RESULT 15  
.AAN70278/c  
ID AAN70278 standard; DNA; 32 BP.  
XX  
XX AAN70278;  
AC  
XX  
XX 03-OCT-2002 (revised)  
DT 26-MAY-1991 (first entry)  
PT  
XX  
XX Sequence of scissile link probe MRC068 (HL).  
DE  
XX  
XX Hybridisation; probe; ss.  
KW  
XX  
XX Synthetic.